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Phylogeny of influenza A(H1)pdm09 viruses, detected in Portugal between 2009 and 2016

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Background:

Influenza A(H1)pdm09 viruses show a constant antigenic pattern since its emergence in the 2009 pandemics. However these viruses have been increasing their genetic diversity. This fact supports the need for continuous monitoring of genetic characteristics of influenza A(H1)pdm09 viruses, which can suddenly acquire new antigenic properties or decrease their susceptibility to antiviral drugs.

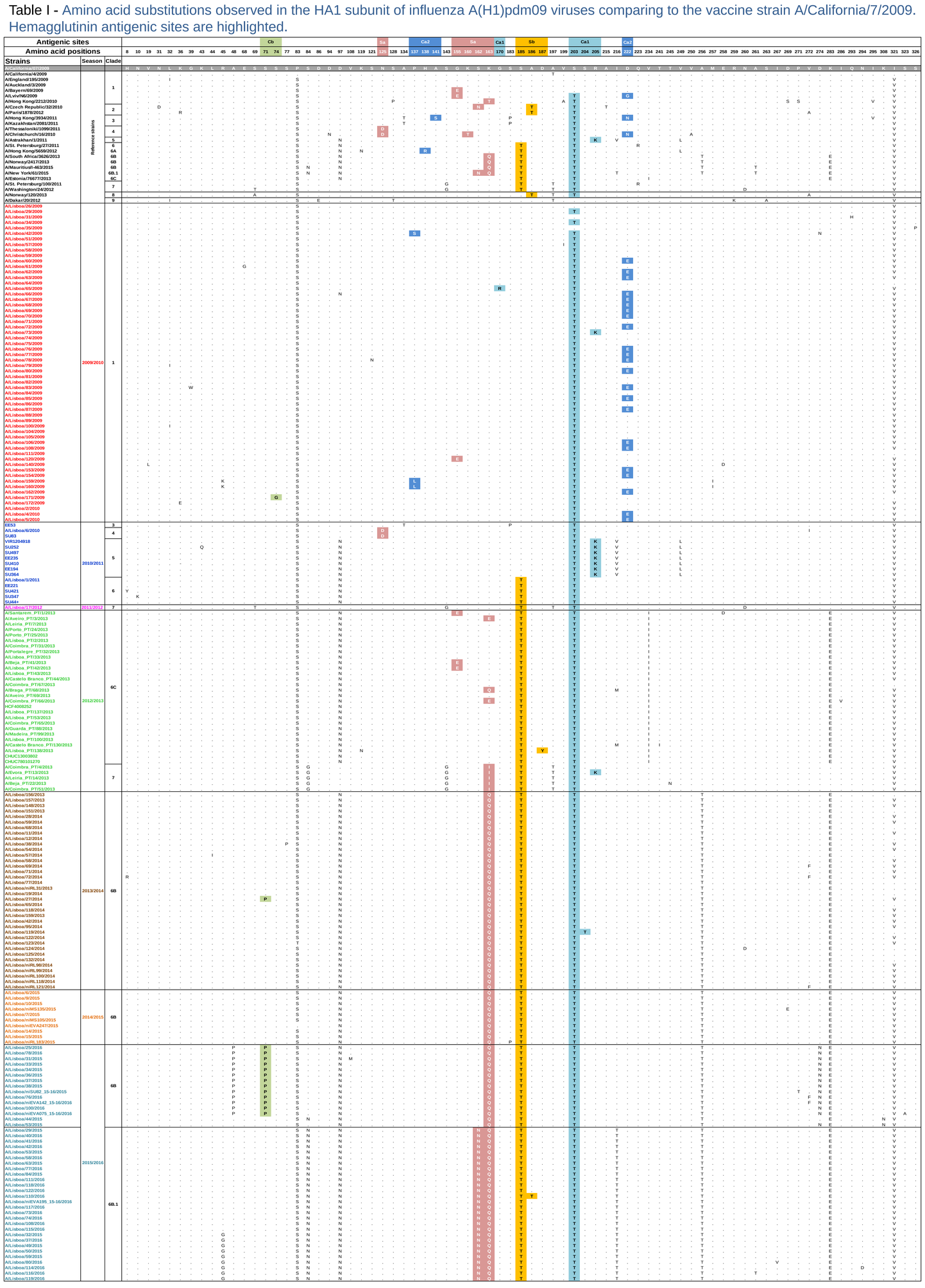
Methods:

From the 2009 pandemic until 2016, the Portuguese NIC has detected 1634 influenza A(H1)pdm09 viruses in the scope of the Portuguese Influenza Surveillance Programme. During this period, 586 viruses were isolated and characterised antigenically by HI assays. Genetic characterisation was also performed for 195 viruses by HA1 subunit sequencing.

Results:

- All studied influenza A(H1)pdm09 viruses revealed no antigenic diversity, being antigenically similar to the vaccine strain A/California/7/2009.
- **2009** - viruses belonged to a single genetic group 1 (A/Hong Kong/2212/2010).
- **2010/2011** - Portuguese pandemic viruses showed genetic diversity, being distributed by 4 genetic groups (3,4,5, and 6), acquiring one or two amino acid changes in antigenic sites.
- **2011/12** - were first detected A(H1)pdm09 from group 7 (A/St. Petersburg/100/2011).
- **2012/13** - majority of circulating viruses belonged to the subgroup 6C (represented by A/Estonia/76677/2013) harbouring 2 amino acid substitutions in antigenic sites of hemagglutinin (S185T and S203T).
- **2013/2014** - all A(H1)pdm09 viruses clustered in the subgroup 6B (A/South Africa/3626/2013) and fixed 3 amino acid changes located in antigenic sites of HA (K163Q, S185T and S203T).
- **2015/2016** - within 6B group, new A(H1)pdm09 viruses have emerged giving rise to a new subgroup 6B.1 represented by the strain A/New York/61/2015. Most viruses presented an additional amino acid substitution in HA antigenic sites: S71P in 6B group and S162N in 6B.1 subgroup.

Table I - Amino acid substitutions observed in the HA1 subunit of influenza A(H1)pdm09 viruses comparing to the vaccine strain A/California/7/2009. Hemagglutinin antigenic sites are highlighted.



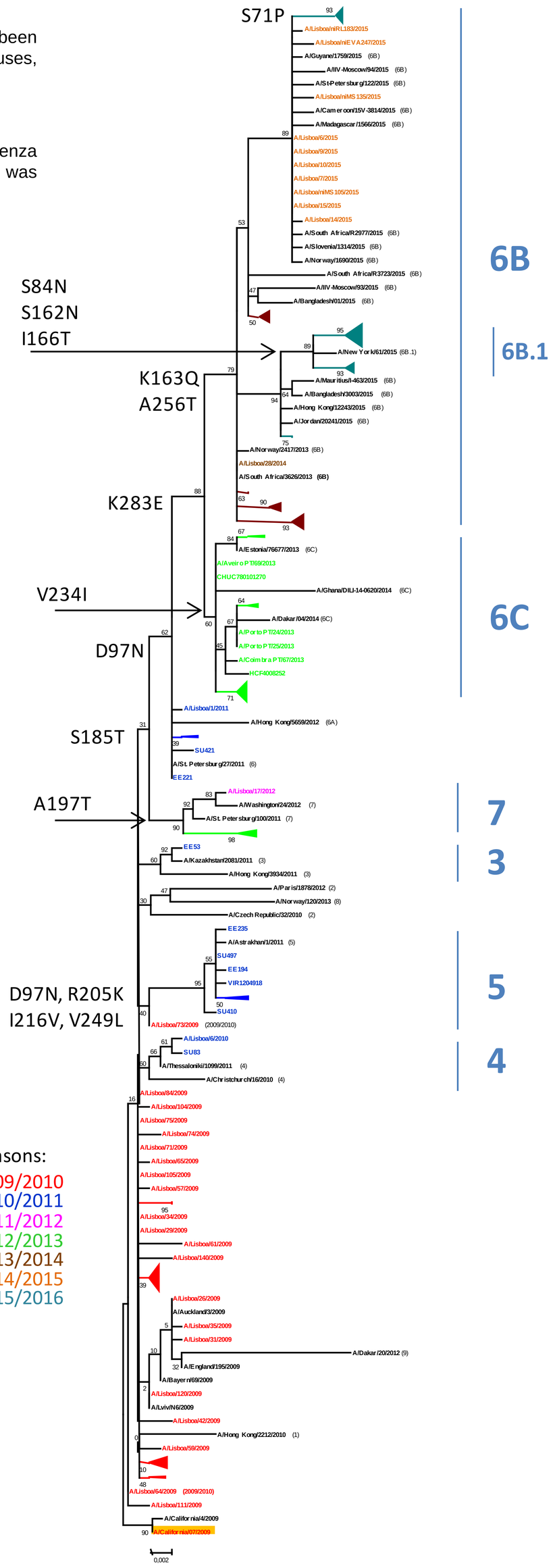


Figure 1 – Maximum likelihood phylogenetic tree of HA1 nucleotide sequences from influenza A(H1)pdm09 viruses, detected in Portugal since the 2009 pandemic until the 2015/2016 winter season. Bootstrap values above 50 are shown (500 replicates). Strains analysed are represented by different colours according to the season of detection: red (2009/2010), blue (2010/2011), pink (2011/2012), green (2012/2013), brown (2013/2014), orange (2014/2015) and teal blue (2015/2016). The vaccine strain is highlighted in yellow, and the reference strains in black.

Conclusions:

- Most influenza A(H1)pdm09 viruses remain antigenically similar to the H1 vaccine strain - A/California/7/2009.
- A(H1)pdm09 viruses have diversify into different genetic groups with an increasing number of amino acid substitutions in antigenic sites.
- The genetic characterisation is crucial to understand possible pathways of evolution and antigenic drift of these viruses.

For further information on this poster please contact:
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